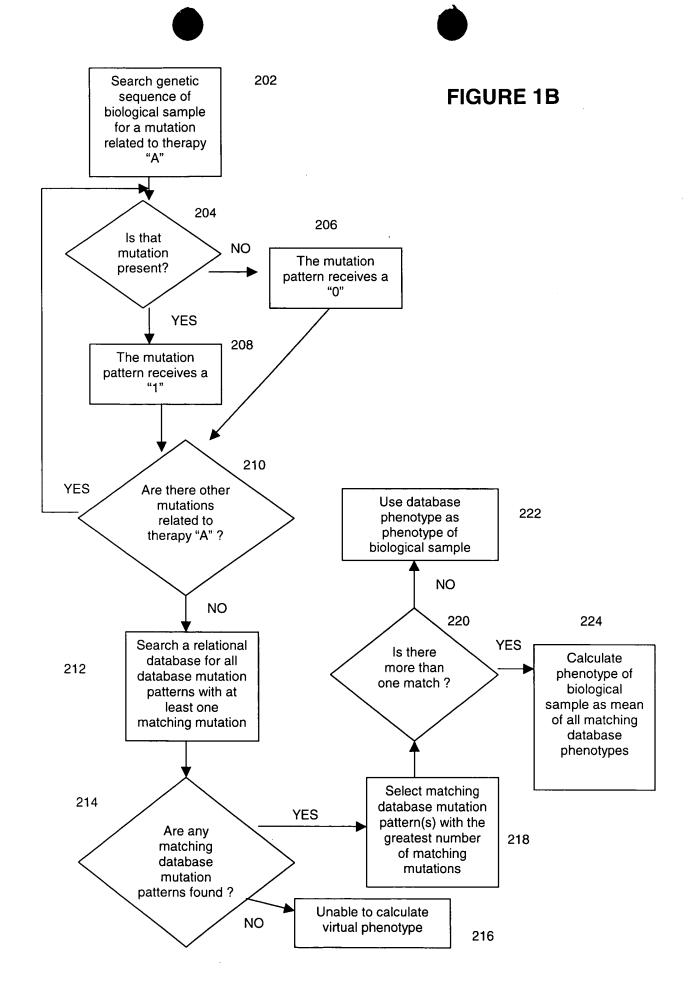


**FIGURE 1A** 



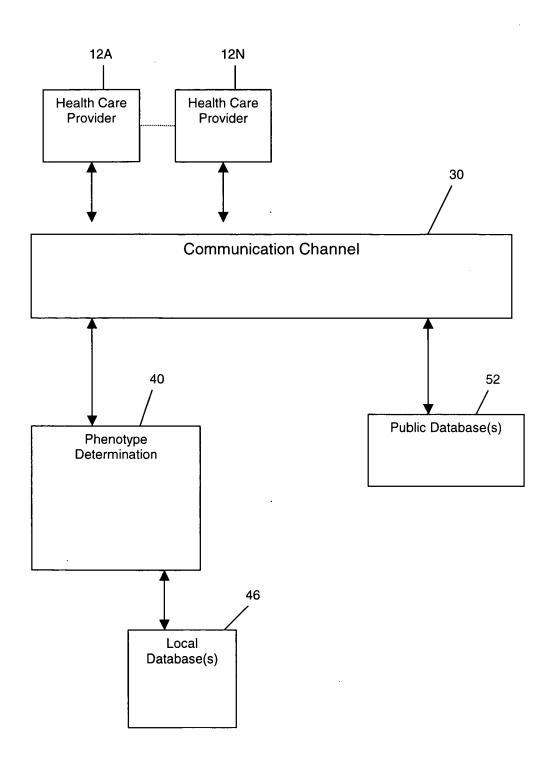
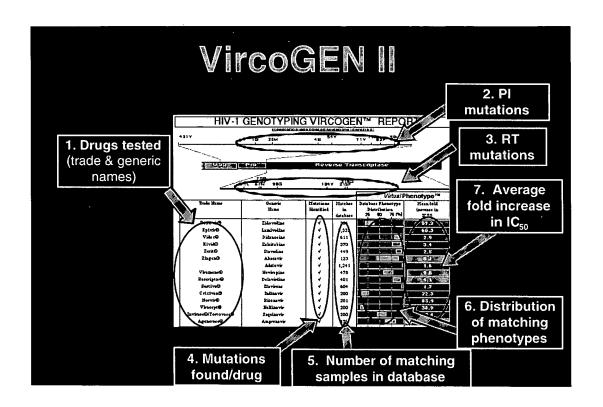


FIGURE 2



# HIV-1 GENOTYPING VIRCOGENTM REPORT Besistance-Associated Mutations identified: 101 461 771 90M 101 Pro Reverse Transcriptase

103N

190A 2190 181C 215Y

				<i>Virtual</i> Phenotype™		
Trade Name	Generic Name	Mutations Identified	Matches in database	Database Phenotype Distribution 25 50 75 (%)	Mean fold increase in IC50	
Retrovir®	Zidovudine		132		73.6	
Epivir®	Lamivudine	٧	874	7755	F. 49.65	
Videx@	Didanosine	<b>1 1</b>	585		1.8	
Hivid®	Zalcitabine	1	329		1.5	
Zerit@	Stavudine	\ \d	549		3.7	
Ziagen®	Abacavir	1	33		2.3	
	Adefovir	1	1,010		2.2	
Viramune®.	Nevirapine	1	108		138.0	
Rescriptor®	Delavirdine	1	102		162.0	
Sustiva®	Bfavirenz	1	97		267.3	
Crixivan@	Indinavir	1	303		13.0	
Norvir®	Ritonavir	√	'301		15.2	
Viracept®	Nelfinavir	1	302		29.5	
Invirase®/Fortovase®	Saquinavir	1	301		160 N 27. 12 Jan	
Agenerase®	Amprenavir	1	215		3.1	

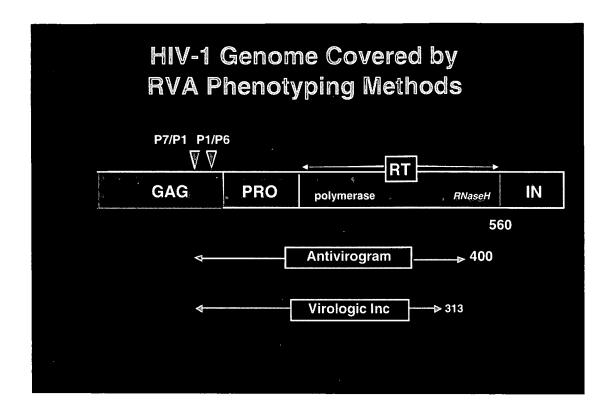
## Virtual & Actual phenotypes

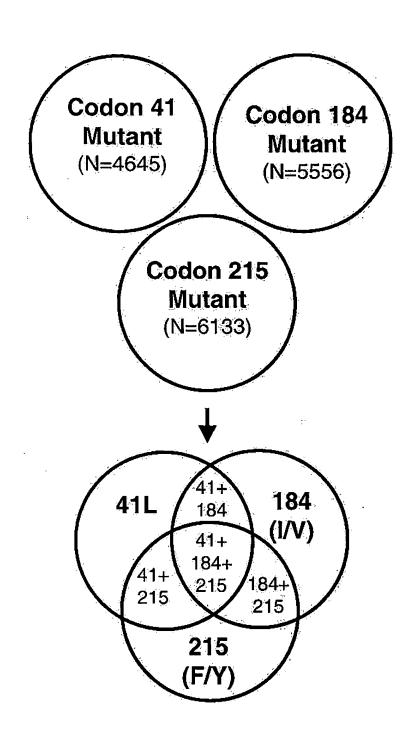
	Matches in Database	Database Pheno spread 25% 50% 75%	Median fold increase in IC50	Actual Phenotype
Indinavir	139	Z	13x	. 17x
Ritonavir	139		115x	179x
Nelfinavir	139		17x	63x
Saquinavir	139		30x	32x
Amprenavir	139		5x	7.5x

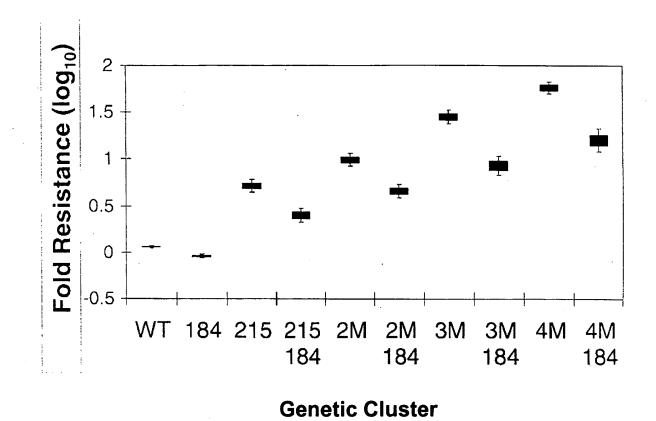
## Overall Concordance

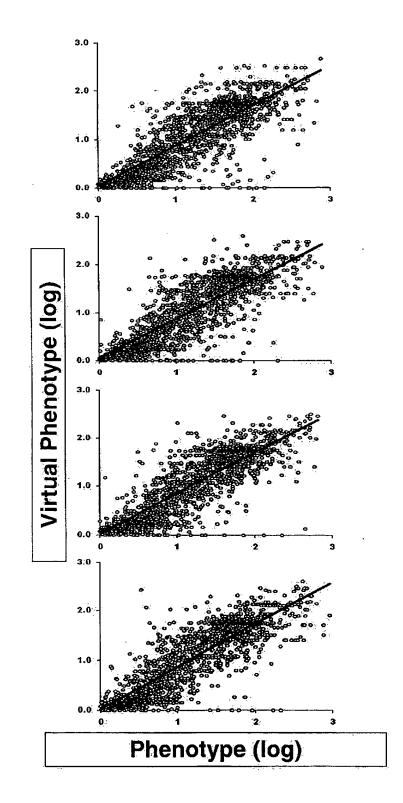
## • 10,000 Samples:

- -Complete concordance: 90 94%
- -Partial concordance: 6 9%
- -Discordance: <1%

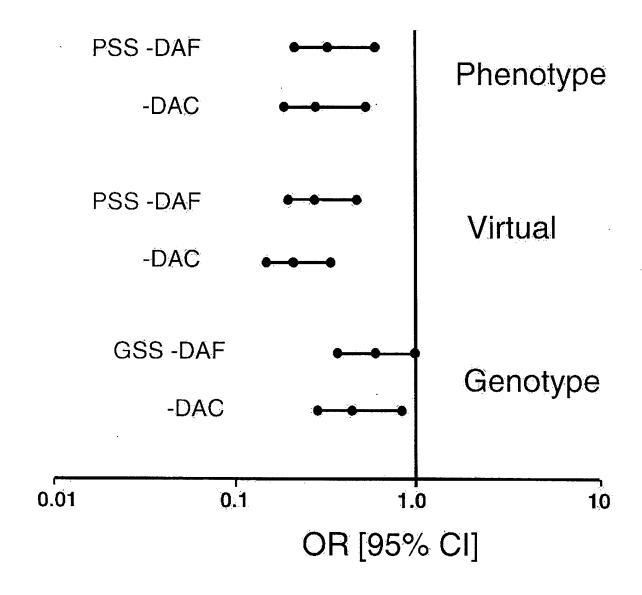


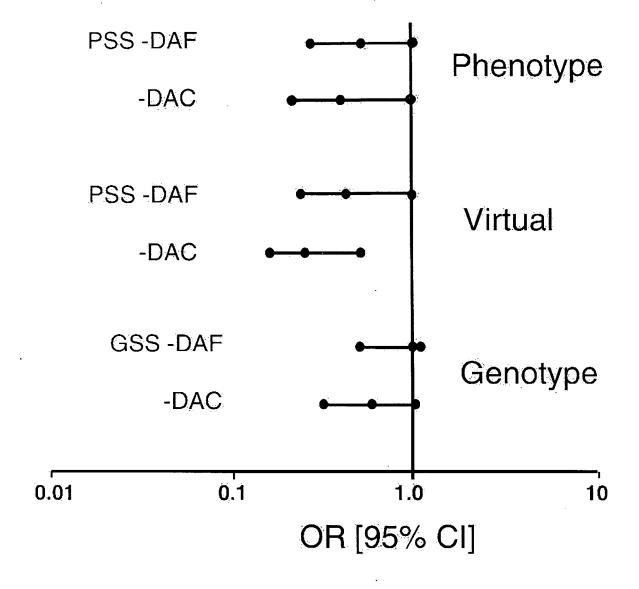






that the test could be the source or of the start of the





The state of the s